IN THE SPECIFICATION:

Kindly amend the specification as shown in the replacement paragraphs below.

Please replace the paragraph beginning at page 34, line 6, with the following substitute paragraph:

Thus, the present invention includes analogs of peptide or protein antigens and co-stimulatory proteins encoded by nucleotide sequences that share substantial sequence identity or homology to corresponding sequences of native or homologous peptide or protein antigens and co-stimulatory proteins disclosed herein. For substantial sequence identity or homology the analog-encoding polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 90 percent sequence identity, and more preferably at least 95 percent sequence identity compared to a corresponding sequence of the native peptide or protein. The comparison is made to a reference sequence over a comparison window of at least 20 nucleotide positions, frequently over a window of at least 25-50 nucleotides, wherein the percentage of sequence identity is calculated by comparing the reference sequence to the polynucleotide sequence, which may include deletions or additions which total 20 percent or less of the reference sequence over the window of comparison. The reference sequence may be a subset of a larger sequence, for example, as a segment of a murine or human B7-1, B7-2, B7-3, B7H, ICAM1, ICAM2, LFA1 or LFA2~~CAP-3~~ sequence described herein. Optimal alignment of sequences for aligning a comparison window may be conducted according to the local homology algorithm of Smith and Waterman, Adv. Appl. Math. 2:482, 1981 by the homology alignment algorithm of Needleman and Wunsch, J. Mol. Biol. 48:443, 1970, by the search for similarity method of Pearson and Lipman, Proc. Natl. Acad. Sci. USA 85:2444, 1988 or by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics

Software Package Release 7.0, Genetics Computer Group, 575 Science Dr., Madison, WI).

Please replace the paragraph beginning at page 35, line 20, with the following substitute paragraph:

To prepare a cDNA library, mRNA is isolated from tissue such as human placenta which expresses ~~CAP-3~~ **the** protein. cDNA is prepared from the mRNA and ligated into a recombinant vector. The vector is transfected into a recombinant host for propagation, screening and cloning. Methods for making and screening cDNA libraries are well known. See Gubler and Hoffman Gene 25:263-269, 1983 and Sambrook, *et al.*, supra.

Please replace the paragraph beginning at page 36, line 3, with the following substitute paragraph:

DNA encoding a peptide or protein antigen or co-stimulatory protein of interest is identified in either cDNA or genomic libraries by its ability to hybridize with nucleic acid probes, for example on Southern blots, and these DNA regions are isolated by standard methods familiar to those of skill in the art. See Sambrook, *et al.* Various methods of amplifying target sequences, such as the polymerase chain reaction, can also be used to prepare nucleic acids encoding peptide or protein antigens and co-stimulatory proteins. PCR technology is used to amplify such nucleic acid sequences directly from mRNA, from cDNA, and from genomic libraries or cDNA libraries. The isolated sequences encoding ~~CAP-3~~ **the** protein may also be used as templates for PCR amplification.